



568.1D1.TXT

SEQUENCE LISTING

<110> Madison, Edwin L

<120> TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA)
VARIANTS: COMPOSITIONS AND METHODS OF USE

<130> TSRI 568.1D1

<140> US 10/705,633

<141> 2003-11-10

<150> US 09/600,985

<151> 2000-11-13

<150> PCT/US97/20226

<151> 1997-11-12

<150> US 60/030,655

<151> 1996-11-12

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 527

<212> PRT

<213> Homo sapiens

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			20					25					30		
Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser	Val	Pro	Val
		35					40					45			
Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Gln	Gln
	50					55					60				
Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	Gly	Phe	Ala
65					70					75				80	
Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	Glu	Asp	Gln
				85					90					95	
Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu
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Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly
		115					120					125			
Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys
		130				135					140				
Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala
145					150					155					160
Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly
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Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His
			180					185					190		
Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile
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210                215                220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
225                230                235
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
245                250                255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
260                265                270
Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
275                280                285
Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
290                295                300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
305                310                315
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
325                330                335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
340                345                350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
355                360                365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
370                375                380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
385                390                395
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
405                410                415
Asp Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
420                425                430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
435                440                445
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
450                455                460
Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465                470                475
Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
485                490                495
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<210> 2

<211> 527

<212> PRT

<213> Homo sapiens

<400> 2

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Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
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Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
20          25          30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
35          40          45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
50          55          60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65          70          75          80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln

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Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu																		
			100						105																								
Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly																		
			115						120																								
Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys																		
			130						135																								
Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala																		
			145						150																								
Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly																		
			165						170																								
Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His																		
			180						185																								
Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile																		
			195						200																								
Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu																		
			210						215																								
Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys																		
			225						230																								
Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys																		
			245						250																								
Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro																		
			260						265																								
Gln	Phe	Glu	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	Ser	His	Pro																		
			275						280																								
Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	Gly	Glu	Arg																		
			290						295																								
Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	Leu	Ser	Ala																		
			305						310																								
Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu	Thr	Val	Ile																		
			325						330																								
Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	Gln	Lys	Phe																		
			340						345																								
Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	Asp	Thr	Tyr																		
			355						360																								
Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	Ser	Arg	Cys																		
			370						375																								
Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	Pro	Ala	Asp																		
			385						390																								
Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	Tyr	Gly	Lys																		
			405						410																								
Glu	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	Glu	Ala	His																		
			420						425																								
Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His	Leu	Leu	Asn																		
			435						440																								
Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly																		
			450						455																								
Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly																		
			465						470																								
Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile																		
			485						490																								
Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr																		
			500						505																								
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<210> 3
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<212> PRT

<213> Homo sapiens

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Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
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Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
      20           25           30
Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
      35           40           45
Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
      50           55           60
Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
      65           70           75           80
Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
      85           90           95
Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
      100          105          110
Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
      115          120          125
Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
      130          135          140
Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
      145          150          155          160
Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
      165          170          175
Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
      180          185          190
Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
      195          200          205
Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
      210          215          220
Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
      225          230          235          240
Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
      245          250          255
Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
      260          265          270
Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
      275          280          285
Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
      290          295          300
Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
      305          310          315          320
Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
      325          330          335
Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
      340          345          350
Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
      355          360          365
Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
      370          375          380
Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
      385          390          395          400
Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
      405          410          415
His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Tyr Glu Ala His
      420          425          430
Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn

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		435				440				445					
Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly
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Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
465					470					475					480
Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile
				485					490					495	
Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr
			500					505					510		
Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met	Arg	Pro	
		515					520					525			

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<210> 4
<211> 290
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<213> Homo sapiens
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caacatgctg	tgtgctggag	acactcggag	cggcggtccc	caggcaaact	tgcacgacgc	180
gtgccagggc	gattcgggag	gccccctggt	gtgctggaac	gatggccgca	tgactttggt	240
cggcacatc	agctggggcc	tgggctgtgg	acagaaggat	gtcccggtg		290

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<212> DNA
<213> Homo sapiens
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caacatgctg	tgtgctggag	acactcggag	cggcgcgccc	caggcaaact	tgcacgacgc	180	
ctgccagggc	gattcgggag	gccccctggt	gtgtctgaac	gatggccgca	tgactttggt	240	
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<213> Homo sapiens
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caacatgctg	tgtgctggag	acactcggag	cggcgctgcc	caggcaaact	tgcacgacgc	180
ctgccagggc	gattcgggag	gccccctggt	gtgcttgaac	gatggccgca	tgactttggt	240
gggcatcatc	agctggggcc	tgggctgtgg	acagaaggat	gtcccgggtg		290

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caacatgctg	tgtgtctggag	acactcggag	cggtcggtccc	caggcaaaat	tgcacgacgc	180
ctgccagggc	gatttcgggaq	gcctccctggt	gtgtctgaac	gatggccgca	tgaactttggt	240

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<211> 23
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          Met Asp Ala Met Lys Arg Gly Leu Cys
          -35                    -30

tgt gtg ctg ctg ctg tgt gga gca gtc ttc gtt tcg ccc agc cag gaa 160
Cys Val Leu Leu Leu Cys Gly Ala Val Phe Val Ser Pro Ser Gln Glu
-25                    -20                    -15

atc cat gcc cga ttc aga aga gga gcc aga tct tac caa gtg atc tgc 208
Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr Gln Val Ile Cys
-10                    -5                    1                    5

aga gat gaa aaa acg cag atg ata tac cag caa cat cag tca tgg ctg 256
Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp Leu
          10                    15                    20

cgc cct gtg ctc aga agc aac cgg gtg gaa tat tgc tgg tgc aac agt 304
Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser
          25                    30                    35

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ggc agg gca cag tgc cac tca gtg cct gtc aaa agt tgc agc gag cca 352
Gly Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro
40 45 50

agg tgt ttc aac ggg ggc acc tgc cag cag gcc ctg tac ttc tca gat 400
Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp
55 60 65 70

ttc gtg tgc cag tgc ccc gaa gga ttt gct ggg aag tgc tgt gaa ata 448
Phe Val Cys Gln Cys Pro Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile
75 80 85

gat acc agg gcc acg tgc tac gag gac cag ggc atc agc tac agg ggc 496
Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln Gly Ile Ser Tyr Arg Gly
90 95 100

acg tgg agc aca gcg gag agt ggc gcc gag tgc acc aac tgg aac agc 544
Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys Thr Asn Trp Asn Ser
105 110 115

agc gcg ttg gcc cag aag ccc tac agc ggg cgg agg cca gac gcc atc 592
Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp Ala Ile
120 125 130

agg ctg ggc ctg ggg aac cac aac tac tgc aga aac cca gat cga gac 640
Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
135 140 145 150

tca aag ccc tgg tgc tac gtc ttt aag gcg ggg aag tac agc tca gag 688
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu
155 160 165

ttc tgc agc acc cct gcc tgc tct gag gga aac agt gac tgc tac ttt 736
Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe
170 175 180

ggg aat ggg tca gcc tac cgt ggc acg cac agc ctc acc gag tcg ggt 784
Gly Asn Gly Ser Ala Tyr Arg Gly Thr His Ser Leu Thr Glu Ser Gly
185 190 195

gcc tcc tgc ctc ccg tgg aat tcc atg atc ctg ata ggc aag gtt tac 832
Ala Ser Cys Leu Pro Trp Asn Ser Met Ile Leu Ile Gly Lys Val Tyr
200 205 210

aca gca cag aac ccc agt gcc cag gca ctg ggc ctg ggc aaa cat aat 880
Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu Gly Lys His Asn
215 220 225 230

tac tgc cgg aat cct gat ggg gat gcc aag ccc tgg tgc cac gtg ctg 928
Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His Val Leu
235 240 245

aag aac cgc agg ctg acg tgg gag tac tgt gat gtg ccc tcc tgc tcc 976
Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
250 255 260

acc tgc ggc ctg aga cag tac agc cag cct cag ttt cgc atc aaa gga 1024
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly

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265					270					275					
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Gly Leu Phe Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe															
280 285 290															
gcc aag cac agg agg tcg ccc gga gag cgg ttc ctg tgc ggg ggc ata	1120														
Ala Lys His Arg Arg Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile															
295 300 305 310															
ctc atc agc tcc tgc tgg att ctc tct gcc gcc cac tgc ttc cag gag	1168														
Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala Ala His Cys Phe Gln Glu															
315 320 325															
agg ttt ccg ccc cac cac ctg acg gtg atc ttg ggc aga aca tac cgg	1216														
Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg															
330 335 340															
gtg gtc cct ggc gag gag gag cag aaa ttt gaa gtc gaa aaa tac att	1264														
Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile															
345 350 355															
gtc cat aag gaa ttc gat gat gac act tac gac aat gac att gcg ctg	1312														
Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu															
360 365 370															
ctg cag ctg aaa tcg gat tcg tcc cgc tgt gcc cag gag agc agc gtg	1360														
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val															
375 380 385 390															
gtc cgc act gtg tgc ctt ccc ccg gcg gac ctg cag ctg ccg gac tgg	1408														
Val Arg Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp															
395 400 405															
acg gag tgt gag ctc tcc ggc tac ggc aag cat gag gcc ttg tct cct	1456														
Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro															
410 415 420															
ttc tat tcg gag cgg ctg aag gag gct cat gtc aga ctg tac cca tcc	1504														
Phe Tyr Ser Glu Arg Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser															
425 430 435															
agc cgc tgc aca tca caa cat tta ctt aac aga aca gtc acc gac aac	1552														
Ser Arg Cys Thr Ser Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn															
440 445 450															
atg ctg tgt gct gga gac act cgg agc ggc ggg ccc cag gca aac ttg	1600														
Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu															
455 460 465 470															
cac gac gcc tgc cag ggc gat tcg gga ggc ccc ctg gtg tgt ctg aac	1648														
His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Asn															
475 480 485															
gat ggc cgc atg act ttg gtg ggc atc atc agc tgg ggc ctg ggc tgt	1696														
Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys															
490 495 500															
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Gly Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu
 505 510 515

gac tgg att cgt gac aac atg cga ccg tga ccaggaacac ccgactcctc 1794
 Asp Trp Ile Arg Asp Asn Met Arg Pro *
 520 525

aaaagcaaat gagatcccgc ctcttcttct tcagaagaca ctgcaaaggc gcagtgtctc 1854
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 gaagagtgc ttttcccaga tacttcccat tttggaagtt ttcaggactt ggtctgattt 1974
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 -15 -10 -5
 Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
 1 5 10
 Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
 15 20 25
 Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
 30 35 40 45
 Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
 50 55 60
 Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
 65 70 75
 Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
 80 85 90
 Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
 95 100 105
 Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
 110 115 120 125
 Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
 130 135 140
 Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
 145 150 155
 Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
 160 165 170
 Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
 175 180 185

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Gly	Thr	His	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	190	195	200	205
Ser	Met	Ile	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	210	215	220	225
Gln	Ala	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	230	235	240	245
Asp	Ala	Lys	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	250	255	260	265
Glu	Tyr	Cys	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	270	275	280	285
Ser	Gln	Pro	Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	290	295	300	305
Ser	His	Pro	Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	310	315	320	325
Gly	Glu	Arg	Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	330	335	340	345
Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu	350	355	360	365
Thr	Val	Ile	Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	370	375	380	385
Gln	Lys	Phe	Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	390	395	400	405
Asp	Thr	Tyr	Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	410	415	420	425
Ser	Arg	Cys	Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	430	435	440	445
Pro	Ala	Asp	Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	450	455	460	465
Tyr	Gly	Lys	His	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	470	475	480	485
Glu	Ala	His	Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His	490	495	500	505
Leu	Leu	Asn	Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	510	515	520	525
Arg	Ser	Gly	Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp				
Ser	Gly	Gly	Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val				
Gly	Ile	Ile	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly				
Val	Tyr	Thr	Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met				
Arg	Pro																		